

Figure 1

09759990 0665260

FIGURE 2

Stability Study of SAHH

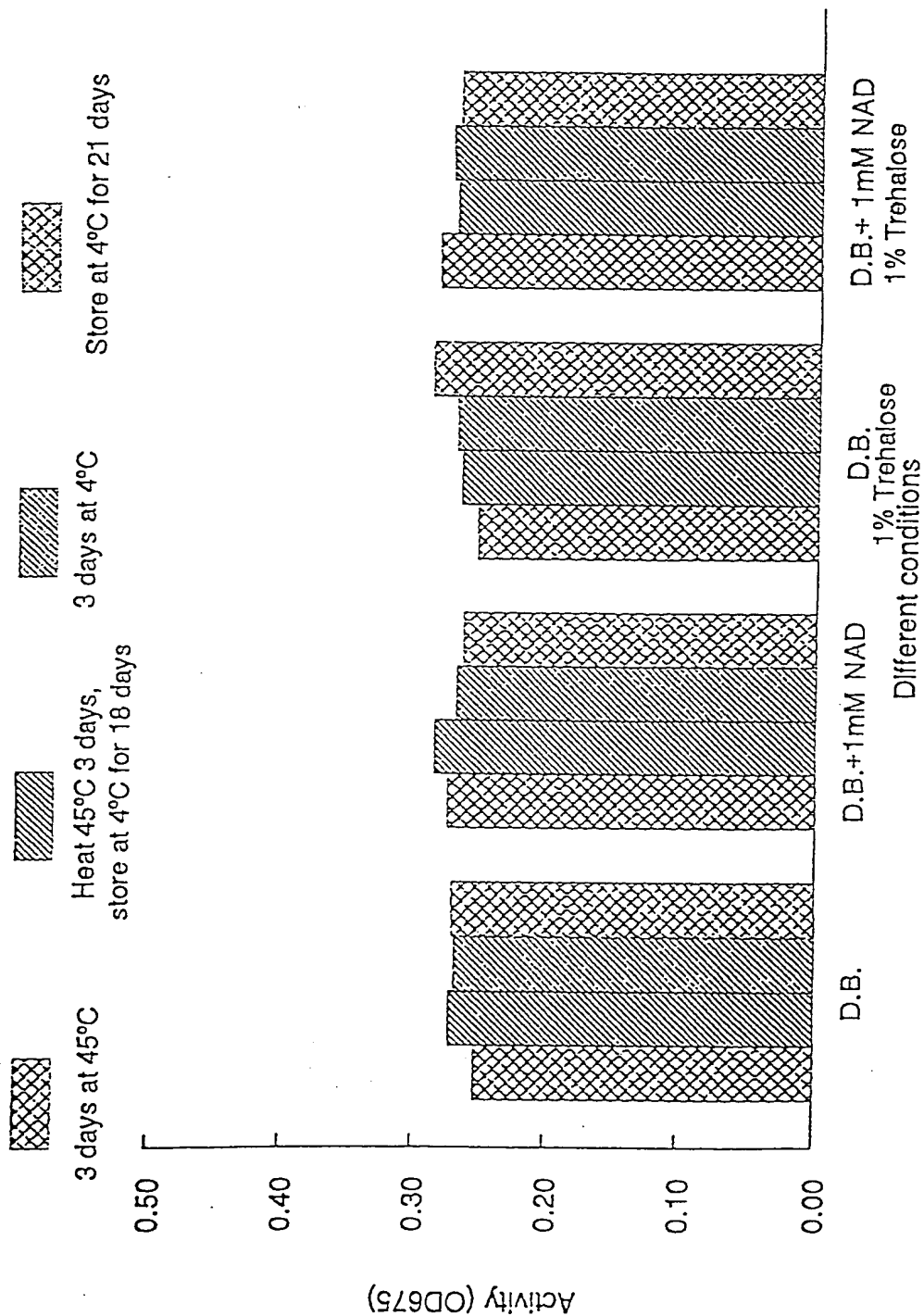


Figure 2

T00E80" 06665260

Screening of SAHH

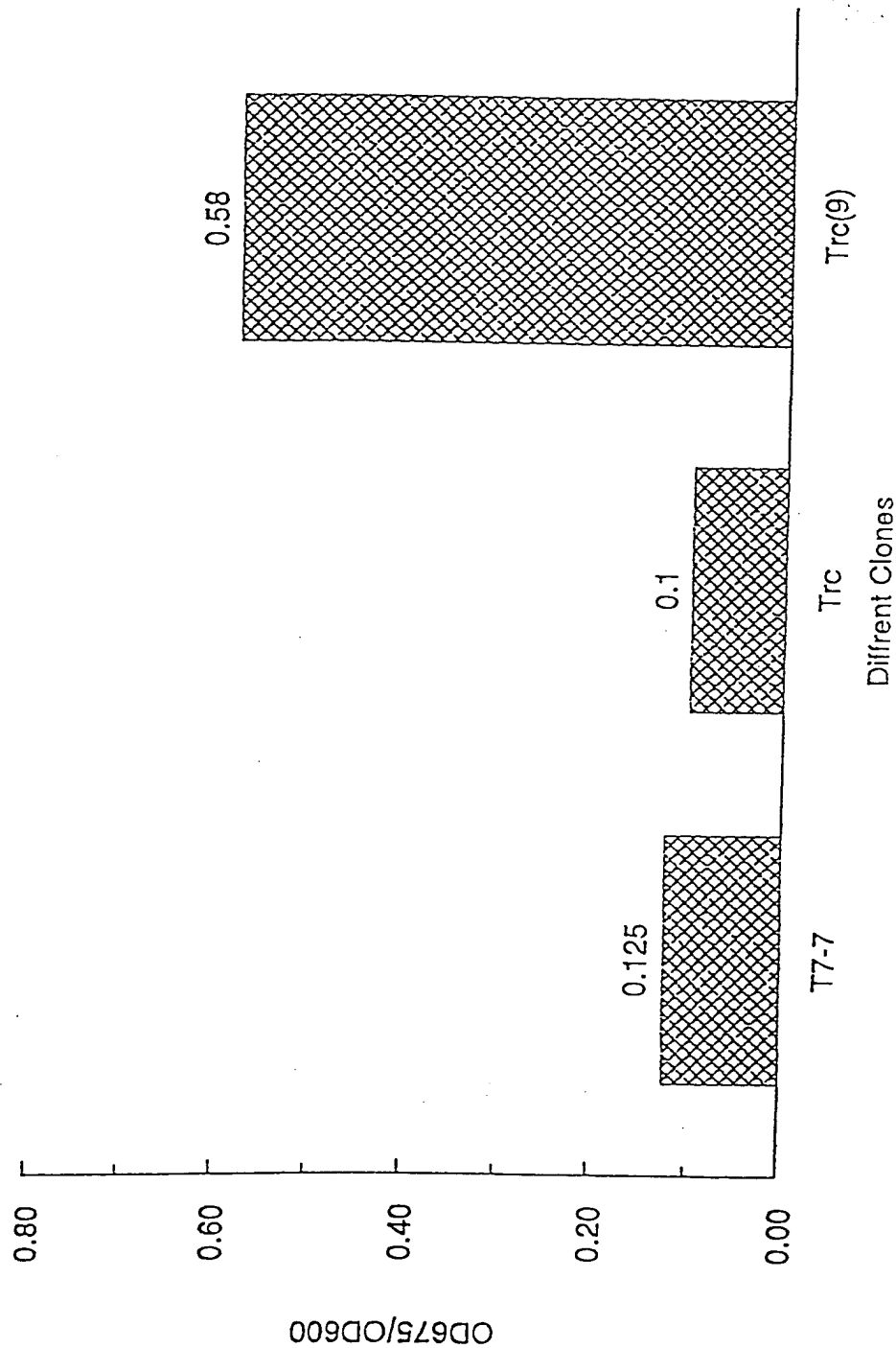


Figure 3

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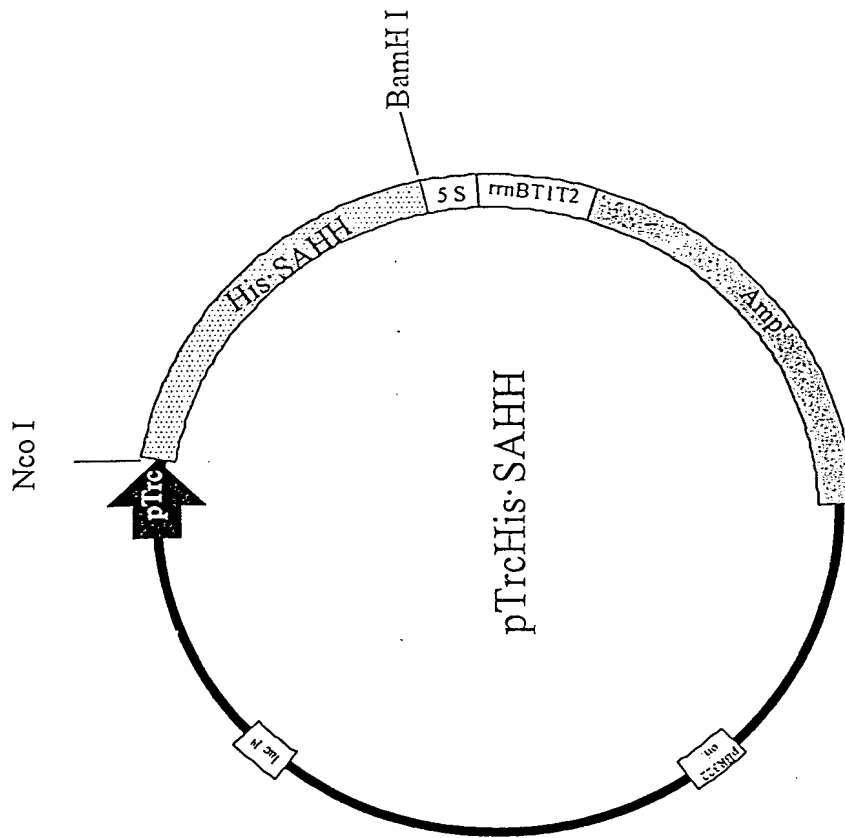


Figure 4

FOIEBO" 06665/60

Stability of SAHH.His

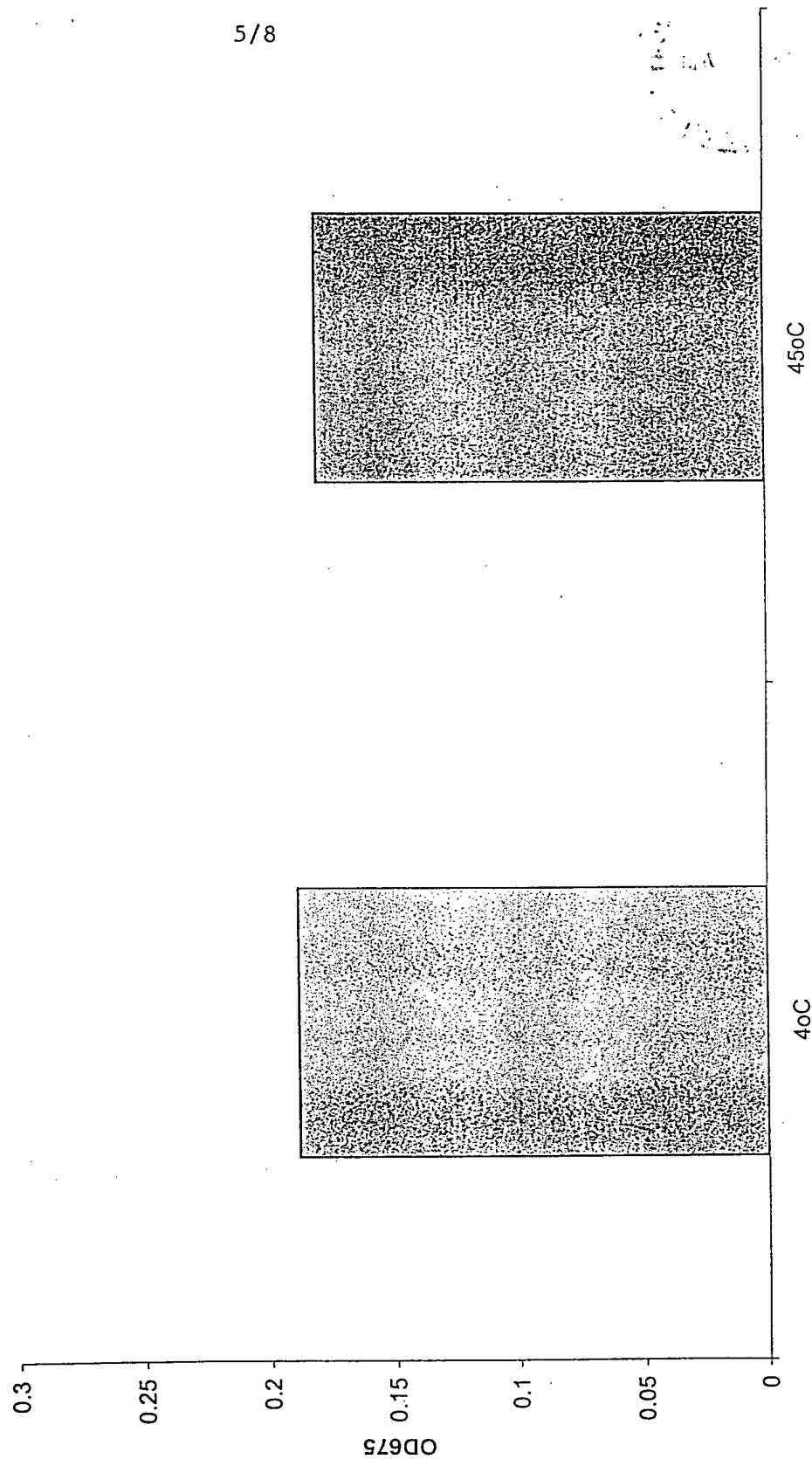


Figure 5

99.2% identity in 1461 residues overlap; Score: 1437.0; Gap frequency: 0.0%

SAHH-wild	291	ATGGCTTGCAAATCACCTGCTGGTGTCTCCATTTCGAGTACAGAATTGCCGACATCAACCTC
A/C,	71	ATGGCTTGCAAATCACCTACTGGTGTCTCCATTTCGAGTACAGAATTGCCGACATCAACCTC

SAHH-wild	351	CATGTTCTCGGCCGTAAGGAACTTACCCCTTGCTGAGAAGGAAATGCCAGGTCTTATGGTT
A/C,	131	CATGTTCTCGGCCGTAAGGAACTTACCCCTTGCTGAGAAGGAAATGCCAGGTCTTATGGTT

SAHH-wild	411	CTTCGTGAGCGTTATTCCGCTTCTAAGCCATTGAAGGGTGTGAGAATCTCTGGTTCCCTC
A/C,	191	CTTCGTGAGCGTTATTCCGCTTCTAAGCCATTGAAGGGTGTGAGAATCTCTGGTTCCCTC

SAHH-wild	471	CACATGACAGTCCAGACAGCGTCTTATTGAGACACTCACAGCTCTTGGTGTGATGTC
A/C,	251	CACATGACAGTCCAGACAGCGTCTTATTGAGACACTCACAGCTCTTGGTGTGATGTC

SAHH-wild	531	AGATGGGCTTCCTGCAACATCTTCTCTACACAAGATACAGCCGCTGCTGCTATCGTTGTC
A/C,	311	AGATGGGCTTCCTGCAACATCTTCTCTACACAAGATACAGCCGCTGCTGCTATCGTTGTC

SAHH-wild	591	GGCCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCAGTCTTCGCCTGGAAGGGCGAA
A/C,	371	GGCCCAACAGGCACACCAGAGAAGCCAGCCGGTATCCAGTCTTCGCCTGGAAGGGCGAA

SAHH-wild	651	ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC
A/C,	431	ACACTCCCAGAATACTGGGAGAACACATACCGCGCTCTCACATGGCCAGATGGTCAAGGC

SAHH-wild	711	CCACAGCAGGTTGTGATGATGGTGGTGTGCTACACTCCTCATCTCCAAGGGCTTCGAA
A/C,	491	CCACAGCAGGTTGTGATGATGGTGGTGTGCTACACTCCTCATCTCCAAGGGCTTCGAA

SAHH-wild	771	TTCGAAACAGCCGGTGTGTTCCAGAGCCAACAGAAGCTGACAACCTCGAATACCGCTGC
A/C,	551	TTCGAAACAGCCGGTGTGTTCCAGAGCCAACAGAAGCTGACAACCTCGAATACCGCTGC

SAHH-wild	831	GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGACAAGAACCACTGGCACACAGTTGCT
A/C,	611	GTTCTTGCTACACTCAAGCAGGTCTTCAACCAAGACAAGAACCACTGGCACACAGTTGCT

SAHH-wild	891	GCCGGCATGAACGGTGTTCCTCCGAGAGACAACAACAGGTGTCCACCGCCTCTACCAGCTC
A/C,	671	GCCGGCATGAACGGTGTTCCTCCGAGAGACAACAACAGGTGTCCACCGCCTCTACCAGCTC

SAHH-wild	951	GAGAAGGAGGGCAAACCTCTTCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC
A/C,	731	GAGAAGGAGGGCAAACCTCTTCCAGCCATCAACGTCAACGACGCTGTTACAAAGTCC

SAHH-wild	1011	AAGTTCGATAACATCTACGGCTGTGCGCACTCCCTTATCGATGGTATCAACCGTGCTTCC
A/C,	791	AAGTTCGATAACATCTACGGCTGTGCGCACTCCCTTATCGATGGTATCAACCGTGCTTCC

SAHH-wild	1071	GATGTCATGATCGGCGGCAAGACAGCTCTCGTCATGGGTTACGGCGATGTCGGGAAGGGC
A/C,	851	GATGTCATGATCGGCGGCAAGACAGCTCTCGTCATGGGTTACGGCGATGTCGGGAAGGGC

SAHH-wild	1131	TGCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCCATC
A/C,	911	TGCGCTCAATCCCTCCGTGGCCAAGGCGCTCGCGTTATCATCACAGAAGTCGACCCAATC

Figure 6a

SAHH-wild 1191 TCGCTCTCCAGGCTGTCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG
A/C, 971 TCGCTCTCCAGGCTGCCATGGAAGGCTACCAGGTCCGCCGCATCGAGGAAGTCGTCAAG

SAHH-wild 1251 GATGTCGATATCTTCGTTACATGCACAGGAACTGCGATATCATCTCTGTTGACATGATG
A/C, 1031 GATGTCGATATCTTCGTTACATGCACAGGAACTGCGATATCATCTCTGTTGACATGATG

SAHH-wild 1311 GCCCAGATGAAGGATAAGGCTATTGTCGGTAACATCGGCCACTTCGATAACGAAATTGAT
A/C, 1091 GCCCAGATGAAGGATAAGGCTATTGTCGGTAACATCGGCCACTTCGATAACGAAATTGAT

SAHH-wild 1371 ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAATACGAC
A/C, 1151 ACAGATGGCCTCATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAATACGAC

SAHH-wildt 1431 ATGTGGGAATTCCCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCTTCTTAAC
A/C, 1211 ATGTGGGAATTCCCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCTTCTTAAC

SAHH-wild 1491 CTTGGTTGCGCTACAGGTCACCCATCTTTCGTTATGTCAATGTCATTACAAAACCAGACA
A/C, 1271 CTTGGCTGCGCTACAGGTCACCCATCTTTCGTTATGTCAATGTCATTACAAAACCAGACA

SAHH-wild 1551 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGATGAAGGTTTACACACTT
A/C, 1331 CTCGCTCAGCTCGACCTCTACGAAAAGAGAGGAAATCTCGAGAAGAAGGTTTACACACTT

SAHH-wild 1611 CCGAAGCATCTCGATGAAGAAGTCGTTTCGCCTCCACCTCGGATCTCTCGATGTCCACCTT
A/C, 1391 CCGAAGCATCTCGATGAAGAAGTCGCTCGCCTCCACCTCGGATCTCTCGATGTCCACCTT

SAHH-wild 1671 ACAAAGCTTACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCCTTACAAG
A/C, 1451 ACAAAGCTTACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCCTTACAAG

SAHH-wild 1731 TCTGATGCTTACCGTTATTAA
A/C, 1511 TCTGATGCTTACCGTTATTAA

65.9% identity in 44 residues overlap; Score: 14.0; Gap frequency: 0.0%

SAHH-wild 782 CGGTGCTGTCCCAGAGCCAACAGAAGCTGACAACCTCGAATACC
A/C, 682 CGGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCTCTACC

80.0% identity in 20 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 1053 GGTATCAACCGTGCTTCCGA
A/C, 674 GGCATGAACGGTGTTTCCGA
** ** *

Figure 6b

87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 564 GATACAGCCGCTGCTG
 A/C, 554 GAAACAGCCGGTGCTG
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64.3% identity in 42 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 1224 GTCCGCCGCATCGAGGAAGTCGTCAAGGATGTCGATATCTTC
 A/C, 710 GTCCACCGCCTCTACCAGCTCGAGAAGGAGGGCAAACCTCCTC
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87.5% identity in 16 residues overlap; Score: 12.0; Gap frequency: 0.0%

SAHH-wild 774 GAAACAGCCGGTGCTG
 A/C, 344 GATACAGCCGCTGCTG
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Figure 6c

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